FIGURE 1

ATG GTCCGGAAAAAGAACCCCCCTCTGAGAAACGTTGCAAGTGAAGGCGAGGGCCAGATCCTGGAGCCTATAGGTACAGAAAGCAAGGTATCTCTGGAGCCTATAGGTACAGAAAGAACAAAGAATTCTCTGCGAGA
TCAGATGTCAGAAAATACGGATCAGAGTGATGCTGCAGAACTAAATCATAAGGAGGAACATAGTTGCATGTTCAAGATCCATCTTCTAGCAGTAGCAGTTGCATGTTCAAGATCCATCTTCTAGCAGTAAGAACGCAGTTC
TGAGTGAGAAGGCTGGCTTCAATTATGAAAGCCCAGTAAGGGAGGAAACTTTCCCTCCTTTCCGCATGATGAGGTGACAGACAGAAATATGTTGGCTTTCTCATTCCAGCTGCTGGG
GGAGTCTGTGAGCCCTTGAGTCTCCGCAAAGAGTCTGCAAGCACAGAGTGGTCAAGCCAATTGTCAAGGTTTGAGCCCAGTTGAGCCCAGTTGCGCTCAAAAAACCCACAAGTGCCTTCAGTGGGGGTGTAAGACTGAATA
GGCTACAGAGGAAACAGGGCAAGCAACAGAGACTGGTCAAGCACAGAGTGGTCAAGCCAATTGTCAAGGTTTGAGCCCAGTTGAGCCCAGTTGCGCTCAAAAAACCCACAAGTGCCTTCAGTGGGGGTGTAAGACTGAATA
AATCCAAAACTGACTTACTGGTGAATGACAACCAGACCCGGCACCTCTGTCTCCAGAGCTTAAATGCAATATCTGTGATATGGTTACTACGGCAACGACCCCACAGAT
CTGATTAAGCACTTCCGAAAGTATCACTTAGGACTGCATAACCGACCAAGATGCTGCATAACCGACCAAGATGCTGCAGTTCAGCCATTCAAAGA
CTTCCAGAAGGTCAACCGTTCTGTGTTTTTCTGGTGGTGCTGCAGGACAATCAATTCTTCAAGGCCTATGATGTGCAGTGACTTCAGGTGGAACATTCATTG
GCATTGGACGGAAAACACCAGATTGCCAAGGAACACCAAGTATTTCCGCTGTAAATTCTGCAAAACCTTCAGTCCTGCACTTCAATCCGTGATTCTGGAGACTTGGGAAAATG
GCAGGACAAGATAACAGTCAAAGCAGGAGATGACAACAGTCTCCTGTTGGGTACTCAGTGCCCATAAAGCCCCTGAGTCCTCTAGACAAAGTGTACAGAGGCCACCAGTTACTACTGGTGTA
AATTTTGTAGTTTCAGCTGTGAGTCATCTAGCTCATTAAACTGCTAGAACATTATGGCAAGCAGCAGTGGTCAGCGGCGGCTAAATCCAGAGTTAAATGATAAGCTTTCC
AGGGGCTCTGTCATTAATCAGAATGATCTAGCAGCCAAAAGTTCAGAGGAGAGAGAACAAGAGCTCGAGTGGGGCTAAAAAGAGGACTTCTCCAGCAAGGGAGCCGA
GGATAATATGGTAACGAGCTATAATTGTCAGTTCTGTGACTTCGTGTCCATTCTGTCTCCAGAGGACTTTGCAGCCCAGAAAGCACCTTGGAGAAATTACTTATCCGTTTGCTTGTGTAGAAAAAGTAATTGTTCCCACTGT
GCACTCTTGCTTCTGCACTTGTCTCCTGGGCGGCTCGCGAGTCAAACATCAGTGCCATCAGTGTCAAACATCAGTGTTCATTGACGCTAGAATGTACTCCTCTTTCACTATGGAAAG
TGTGCATGAGTCCCAAGCATCGGATGTCAAACAAGAAGCAAATCACCTGTGTCAAGGAAAGCAAGAACACTCATGTACCAAATGTGATTTTATTA
CCCAAGTGGAAGAAGAGATTCCCGACATCACTACAGCCAACGCGTTGTGCTCAGTGCAGTTTTACAGCTGCGAGCACTTCAACACTGTT
CACTGCCAGGAACAGGACATCACTACAGCCACCCAGGTGTGTGTCCGTCATGCCAAGAGAAGCTGGAAGAGAAGTTGGACCGAGAGTTCCAGTGATGACCTTCGCAATGTGACTT
TAAAATGGGAGGGCCAGTTTCTGAGAGTGGGGGGAGTCCGTCATACACCCAAGCAAGCCTGGGGCTGCTGCGCGTGTCTGCACCCAAGAGCAGACAAAGACTCTAAGGGATAGTCCCAATGTG
GGAGAGGGGCCAGACATCCTGCGGGGGGAGTCCGTCATACACCCAAGCAAGCCTGGGGCTGCTGCGCGTGTCTGCACCCAAGAGCAGACAAAGACTCTAAGGGATAGTCCCAATGTG
GAGGCCGCCATCTGGCGCGACCTATTTATGGCTTGGTGTGGAAACCAAGGATTCCTGCAGGGGCGCCAGCTGGCGGAGAAGTCTGGGGCCCTCCCCCAGCAGTATCCTGCATC
GGGAGAAACAAGTCCAAGGATGAATCCCAGTCCCTGTTACGGAGGCGTAGAGCGTCCGGTGTTTTTGTGCCAATTGCCTAGGAGGAGAAGAATGCAAATG
GCGGATATGTATGCAACGCGTGTGGCCCTCTACCCAGAAGCTTCACTGAGCTTCCCAGGCCTTAAACATCATTAAACAAACAACCGGTAGGAGAGGAGAACAAGAAAGCGC
CTTAACCCAGAGAAATTCCACTCCCCCAGCCTAAGTAAAATACGAAGCCCAGGGTTCATTGACTAAAGCCATTCGTCCTGGTCAGCCAGCCAGTCGTGATATTCACAAAAGGA
CCAGAGAGAAATTCCACTCCCCCAGCCTAAGTAAAATACGAAGCCCAGGGTTCATTGACTAAAGCCATTCGTCCTGGTCAGCCAGCCAGTCGTGATATTCACAAAAGGA
TGCAACCTTTGCACATTCAGATAAAAGTCCTCAGGAAAGTACTGGAGAATCCTCAGGAAAGTTCTGAAGGAAAATAGTTCATCCGTAATGACTTCTTGAGAGGAGCAGTCCTATAGAAAAGTAC
ATGAGACCTGCGAAACACCCAAATTATTCACCACCAGGAGAATAGTTCAGAGAAGTACCAGTACCCACTTTTGACTTCCCTTTGTACATAATGACTTCCTTATCCACCTTCAATCTGCCTC
GCGGTTCTGAGTAAATATAAGCTCTCCGTTCCGTAGATTTGGCGATCAGAGTGCCGACTACTTGATGACATTCCTTATCCACCTTCAATCTGCCTC
CTCATTTTTCAGCTGTTGGATCAGACAATGACATTCCTTAGATTGGCGATCAGAGTGCCGACTACTTGATGACATTCCTTATCCACCTTCAATCTGCCTC
GTAAAAAATGAAGGTCCCTTGAATGTAGTAGAAACAGAGAAAGTTGATAGAAGTACTCAAGATGAAATGTGTGCACTGTGGCATTGGCACTGTGGTGCTGGGAAGGCACCACCAAAT
TGCTTTGCATATGAGTTGCCATGTGACAGTTGCCAGTGACCTTTCCAGTGCAGCAAATATGCCAGCACATATCCAGAGGGCCTGCATAGGAACA
ATGCACACAAGTGAAAAAATGAAAACCTAAAGAG TAA *

FIGURE 2

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MVRKKNPPLRNVASEGEGQILEPIGTESKVSGKNKEFSADQMSENTDQSDAAELNHKEEHSLHVQDPSSSSKKDLKSAVLSEKAGFNYE
SPSKGGNFPSFPHDEVTDRNMLAFSFPAAGGVCEPLKSPQRAEADDPQDMACTPSGDSLETKEDQKMSPKATEETGQAQSGQANCQGLS
PVSVASKNPQVPSDGGVRLNKSKTDLLVNDNPDPAPLSPELQDFKCNICGYGYYGNDPTDLIKHFRKYHLGLHNRTRQDAELDSKILAL
HNMVQFSHSKDFQKVNRSVFSGVLQDINSSRPVLLNGTYDVQVTSGGTFIGIGRKTPDCQGNTKYFRCKFCNFTYMGNSSTELEQHFLQ
THPNKIKASLPSSEVAKPSEKNSNKSIPALQSSDSGDLGKWQDKITVKAGDDTPVGYSVPIKPLDSSRQNGTEATSYYWCKFCSFSCES
SSSLKLLEHYGKQHGAVQSGGLNPELNDKLSRGSVINQNDLAKSSEGETMTKTDKSSSGAKKKDFSSKGAEDNMVTSYNCQFCDFRYSK
SHGPDVIVVGPLLRHYQQLHNIHKCTIKHCPFCPRGLCSPEKHLGEITYPFACRKSNCSHCALLLLHLSPGAAGSSRVKHQCHQCSFTT
PDVDVLLFHYESVHESQASDVKQEANHLQGSDGQQSVKESKEHSCTKCDFITQVEEEISRHYRRAHSCYKCRQCSFTAADTQSLLEHFN
TVHCQEQDITTANGEEDGHAISTIKEEPKIDFRVYNLLTPDSKMGEPVSESVVKREKLEEKDGLKEKVWTESSSDDLRNVTWRGADILR
GSPSYTQASLGLLTPVSGTQEQTKTLRDSPNVEAAHLARPIYGLAVETKGFLQGAPAGGEKSGALPQQYPASGENKSKDESQSLLRRRR
GSGVFCANCLTTKTSLWRKNANGGYVCNACGLYQKLHSTPRPLNIIKQNNGEQIIRRRTRKRLNPEALQAEQLNKQQRGSNEEQVNGSP
LERRSEDHLTESHQREIPLPSLSKYEAQGSLTKSHSAQQPVLVSQTLDIHKRMQPLHIQIKSPQESTGDPGNSSSVSEGKGSSERGSPI
EKYMRPAKHPNYSPPGSPIEKYQYPLFGLPFVHNDFQSEADWLRFWSKYKLSVPGNPHYLSHVPGLPNPCQNYVPYPTFNLPPHFSAVG
SDNDIPLDLAIKHSRPGPTANGASKEKTKAPPNVKNEGPLNVVKTEKVDRSTQDELSTKCVHCGIVFLDEVMYALHMSCHGDSGPFQCS
ICQHLCTDKYDFTTHIQRGLHRNNAQVEKNGKPKE
```

FIGURE 3A

```
                              1                                                                                                110
original BCY1    (1)   ---GCCGAGCTGCGCCTGCGCCTGAAGGGCAGCAGCAACACCACGGAGTGTGTTCCCGTGCCCACCTCCGAGCACGTGGCCGAGCACGTGGGCCAGGCAGGCAAGGCTGCAAGATTAAGGC
MC50A19 BCY I    (1)   ATGGCCGAGCTGCGCCTGCGCCTGAAGGGCAGCAGCAACACCACGGAGTGTGTTCCCGTGCCCACCTCCGAGCACGTGGCCGAGCACGTGGGCCAGGCAGGCAAGGCTGCAAGATTAAGGC
MC50A6 BCY I     (1)   ATGGCCGAGCTGCGCCTGCGCCTGAAGGGCAGCAGCAACACCACGGAGTGTGTTCCCGTGCCCACCTCCGAGCACGTGGCCGAGCACGTGGGCCAGGCAGGCAAGGCTGCAAGATTAAGGC
MC50A8 BCY I     (1)   ATGGCCGAGCTGCGCCTGCGCCTGAAGGGCAGCAGCAACACCACGGAGTGTGTTCCCGTGCCCACCTCCGAGCACGTGGCCGAGCACGTGGGCCAGGCAGGCAAGGCTGCAAGATTAAGGC
MC54.21 BCY I    (1)   ATGGCCGAGCTGCGCCTGCGCCTGAAGGGCAGCAGCAACACCACGGAGTGTGTTCCCGTGCCCACCTCCGAGCACGTGGCCGAGCACGTGGGCCAGGCAGGCAAGGCTGCAAGATTAAGGC
MC55.29 BCY I    (1)   ATGGCCGAGCTGCGCCTGCGCCTGAAGGGCAGCAGCAACACCACGGAGTGTGTTCCCGTGCCCACCTCCGAGCACGTGGCCGAGCACGTGGGCCAGGCAGGCAAGGCTGCAAGATTAAGGC
MC55.32 BCY I    (1)   ATGGCCGAGCTGCGCCTGCGCCTGAAGGGCAGCAGCAACACCACGGAGTGTGTTCCCGTGCCCACCTCCGAGCACGTGGCCGAGCACGTGGGCCAGGCAGGCAAGGCTGCAAGATTAAGGC
Consensus        (1)   ATGGCCGAGCTGCGCCTGCGCCTGAAGGGCAGCAGCAACACCACGGAGTGTGTTCCCGTGCCCACCTCCGAGCACGTGGCCGAGCACGTGGGCCAGGCAGGCAAGGCTGCAAGATTAAGGC

                              111                                                                                              220
original BCY1  (108)   CTTGAGGGCCAAGACCAACAACCAACACCTACATCAAGACACCGGTGAGGGGCGAGGAACCAGTGTTCATGGTGACAGGCGACGGGACGGTGCCACAGCCCGGCGGGAAATCA
MC50A19 BCY I  (111)   CTTGAGGGCCAAGACCAACAACCAACACCTACATCAAGACACCGGTGAGGGGCGAGGAACCAGTGTTCATGGTGACAGGCGACGGGACGGTGCCACAGCCCGGCGGGAAATCA
MC50A6 BCY I   (111)   CTTGAGGGCCAAGACCAACAACCAACACCTACATCAAGACACCGGTGAGGGGCGAGGAACCAGTGTTCATGGTGACAGGCGACGGGACGGTGCCACAGCCCGGCGGGAAATCA
MC50A8 BCY I   (111)   CTTGAGGGCCAAGACCAACAACCAACACCTACATCAAGACACCGGTGAGGGGCGAGGAACCAGTGTTCATGGTGACAGGCGACGGGACGGTGCCACAGCCCGGCGGGAAATCA
MC54.21 BCY I  (111)   CTTGAGGGCCAAGACCAACAACCAACACCTACATCAAGACACCGGTGAGGGGCGAGGAACCAGTGTTCATGGTGACAGGCGACGGGACGGTGCCACAGCCCGGCGGGAAATCA
MC55.29 BCY I  (111)   CTTGAGGGCCAAGACCAACAACCAACACCTACATCAAGACACCGGTGAGGGGCGAGGAACCAGTGTTCATGGTGACAGGCGACGGGACGGTGCCACAGCCCGGCGGGAAATCA
MC55.32 BCY I  (111)   CTTGAGGGCCAAGACCAACAACCAACACCTACATCAAGACACCGGTGAGGGGCGAGGAACCAGTGTTCATGGTGACAGGCGACGGGACGGTGCCACAGCCCGGCGGGAAATCA
Consensus      (111)   CTTGAGGGCCAAGACCAACAACCAACACCTACATCAAGACACCGGTGAGGGGCGAGGAACCAGTGTTCATGGTGACAGGCGACGGGACGGTGCCACAGCCCGGCGGGAAATCA

                              221                                                                                              330
original BCY1  (218)   TCTCAGCAGCGGAGCACTTCTCCATGATCCGTGCCTCCCGCAACAAGTCAGGCGCCGGCCAGTGACCATCCGTGCGGGTG
MC50A19 BCY I  (221)   TCTCAGCAGCGGAGCACTTCTCCATGATCCGTGCCTCCCGCAACAAGTCAGGCGCCGGCCAGTGACCATCCGTGCGGGTG
MC50A6 BCY I   (221)   TCTCAGCAGCGGAGCACTTCTCCATGATCCGTGCCTCCCGCAACAAGTCAGGCGCCGGCCAGTGACCATCCGTGCGGGTG
MC50A8 BCY I   (221)   TCTCAGCAGCGGAGCACTTCTCCATGATCCGTGCCTCCCGCAACAAGTCAGGCGCCGGCCAGTGACCATCCGTGCGGGTG
MC54.21 BCY I  (221)   TCTCAGCAGCGGAGCACTTCTCCATGATCCGTGCCTCCCGCAACAAGTCAGGCGCCGGCCAGTGACCATCCGTGCGGGTG
MC55.29 BCY I  (221)   TCTCAGCAGCGGAGCACTTCTCCATGATCCGTGCCTCCCGCAACAAGTCAGGCGCCGGCCAGTGACCATCCGTGCGGGTG
MC55.32 BCY I  (221)   TCTCAGCAGCGGAGCACTTCTCCATGATCCGTGCCTCCCGCAACAAGTCAGGCGCCGGCCAGTGACCATCCGTGCGGGTG
Consensus      (221)   TCTCAGCAGCGGAGCACTTCTCCATGATCCGTGCCTCCCGCAACAAGTCAGGCGCCGGCCAGTGACCATCCGTGCGGGTG

                              331                                                                                              440
original BCY1  (328)   CCCTACCGCGTGGTGGGCTGGTGGTGGTGGGCCCCAAAGGGGCAACCATCCAGCAGCAAACCAACCAACATTATCACACACATTAT CACCAAGCCGTGACCGGACCCCGT
MC50A19 BCY I  (331)   CCCTACCGCGTGGTGGGCTGGTGGTGGTGGGCCCCAAAGGGGCAACCATCCAGCAGCAAACCAACCAACATTATCACACACATTATCACCAAGCCGTGACCGGACCCCGT
MC50A6 BCY I   (331)   CCCTACCGCGTGGTGGGCTGGTGGTGGTGGGCCCCAAAGGGGCAACCATCCAGCAGCAAACCAACCAACATTATCACACACATTATCACCAAGCCGTGACCGGACCCCGT
MC50A8 BCY I   (331)   CCCTACCGCGTGGTGGGCTGGTGGTGGTGGGCCCCAAAGGGGCAACCATCCAGCAGCAAACCAACCAACATTATCACACACATTATCACCAAGCCGTGACCGGACCCCGT
MC54.21 BCY I  (331)   CCCTACCGCGTGGTGGGCTGGTGGTGGTGGGCCCCAAAGGGGCAACCATCCAGCAGCAAACCAACCAACATTATCACACACATTATCACCAAGCCGTGACCGGACCCCGT
MC55.29 BCY I  (331)   CCCTACCGCGTGGTGGGCTGGTGGTGGTGGGCCCCAAAGGGGCAACCATCCAGCAGCAAACCAACCAACATTATCACACACATTATCACCAAGCCGTGACCGGACCCCGT
MC55.32 BCY I  (331)   CCCTACCGCGTGGTGGGCTGGTGGTGGTGGGCCCCAAAGGGGCAACCATCCAGCAGCAAACCAACCAACATTATCACACACATTATCACCAAGCCGTGACCGGACCCCGT
Consensus      (331)   CCCTACCGCGTGGTGGGCTGGTGGTGGTGGGCCCCAAAGGGGCAACCATCCAGCAGCAAACCAACCAACATTATCACACACATTATCACCAAGCCGTGACCGGACCCCGT
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FIGURE 3A

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                                                                                                              550
original BCY1  (438)  GTTCGAGATCACGGGTGCCCCAGGCAACGTGGAGCGCTGCGCGCGAGGAGACGCACATCGCGGTGCGCCACTGGCAAGATCCTCGAGTACAACAATGAAAACGACT
MC50A19 BCY I  (441)  GTTCGAGATCACGGGTGCCCCAGGCAACGTGGAGCGCTGCGCGCGAGGAGACGCACATCGCGGTGCGCCACTGGCAAGATCCTCGAGTACAACAATGAAAACGACT
MC50A6 BCY I   (441)  GTTCGAGATCACGGGTGCCCCAGGCAACGTGGAGCGCTGCGCGCGAGGAGACGCACATCGCGGTGCGCCACTGGCAAGATCCTCGAGTACAACAATGAAAACGACT
MC50A8 BCY I   (441)  GTTCGAGATCACGGGTGCCCCAGGCAACGTGGAGCGCTGCGCGCGAGGAGACGCACATCGCGGTGCGCCACTGGCAAGATCCTCGAGTACAACAATGAAAACGACT
MC54.21 BCY I  (441)  GTTCGAGATCACGGGTGCCCCAGGCAACGTGGAGCGCTGCGCGCGAGGAGACGCACATCGCGGTGCGCCACTGGCAAGATCCTCGAGTACAACAATGAAAACGACT
MC55.29 BCY I  (441)  GTTCGAGATCACGGGTGCCCCAGGCAACGTGGAGCGCTGCGCGCGAGGAGACGCACATCGCGGTGCGCCACTGGCAAGATCCTCGAGTACAACAATGAAAACGACT
MC55.32 BCY I  (441)  GTTCGAGATCACGGGTGCCCCAGGCAACGTGGAGCGCTGCGCGCGAGGAGACGCACATCGCGGTGCGCCACTGGCAAGATCCTCGAGTACAACAATGAAAACGACT
Consensus      (441)  GTTCGAGATCACGGGTGCCCCAGGCAACGTGGAGCGCTGCGCGCGAGGAGACGCACATCGCGGTGCGCCACTGGCAAGATCCTCGAGTACAACAATGAAAACGACT

                                                                                                              660
original BCY1  (548)  TCCTGGCGGGGAGCCCCGACGCAGCAGCAATCGATAGCCGCTACTCCGACGCCGGTGCCGGTGCCCGGCTGCAAGCCCCTCGACCTTCCGGCAGAACAGCCTGGGC
MC50A19 BCY I  (551)  TCCTGGCGGGGAGCCCCGACGCAGCAGCAATCGATAGCCGCTACTCCGACGCCGGTGCCGGTGCCCGGCTGCAAGCCCCTCGACCTTCCGGCAGAACAGCCTGGGC
MC50A6 BCY I   (551)  TCCTGGCGGGGAGCCCCGACGCAGCAGCAATCGATAGCCGCTACTCCGACGCCGGTGCCGGTGCCCGGCTGCAAGCCCCTCGACCTTCCGGCAGAACAGCCTGGGC
MC50A8 BCY I   (551)  TCCTGGCGGGGAGCCCCGACGCAGCAGCAATCGATAGCCGCTACTCCGACGCCGGTGCCGGTGCCCGGCTGCAAGCCCCTCGACCTTCCGGCAGAACAGCCTGGGC
MC54.21 BCY I  (551)  TCCTGGCGGGGAGCCCCGACGCAGCAGCAATCGATAGCCGCTACTCCGACGCCGGTGCCGGTGCCCGGCTGCAAGCCCCTCGACCTTCCGGCAGAACAGCCTGGGC
MC55.29 BCY I  (551)  TCCTGGCGGGGAGCCCCGACGCAGCAGCAATCGATAGCCGCTACTCCGACGCCGGTGCCGGTGCCCGGCTGCAAGCCCCTCGACCTTCCGGCAGAACAGCCTGGGC
MC55.32 BCY I  (551)  TCCTGGCGGGGAGCCCCGACGCAGCAGCAATCGATAGCCGCTACTCCGACGCCGGTGCCGGTGCCCGGCTGCAAGCCCCTCGACCTTCCGGCAGAACAGCCTGGGC
Consensus      (551)  TCCTGGCGGGGAGCCCCGACGCAGCAGCAATCGATAGCCGCTACTCCGACGCCGGTGCCGGTGCCCGGCTGCAAGCCCCTCGACCTTCCGGCAGAACAGCCTGGGC

                                                                                                              770
original BCY1  (658)  TGCATCGGCGAGTGCGAGTGGACTCTGCCTTTGAGGCCCCACGCCGGGGACTTTGGCTACGCGGGGACTCTTTCCGGGGCTATGGCGTGGGCAA
MC50A19 BCY I  (661)  TGCATCGGCGAGTGCGAGTGGACTCTGCCTTTGAGGCCCCACGCCGGGGACTTTGGCTACGCGGGGACTCTTTCCGGGGCTATGGCGTGGGCAA
MC50A6 BCY I   (661)  TGCATCGGCGAGTGCGAGTGGACTCTGCCTTTGAGGCCCCACGCCGGGGACTTTGGCTACGCGGGGACTCTTTCCGGGGCTATGGCGTGGGCAA
MC50A8 BCY I   (661)  TGCATCGGCGAGTGCGAGTGGACTCTGCCTTTGAGGCCCCACGCCGGGGACTTTGGCTACGCGGGGACTCTTTCCGGGGCTATGGCGTGGGCAA
MC54.21 BCY I  (661)  TGCATCGGCGAGTGCGAGTGGACTCTGCCTTTGAGGCCCCACGCCGGGGACTTTGGCTACGCGGGGACTCTTTCCGGGGCTATGGCGTGGGCAA
MC55.29 BCY I  (661)  TGCATCGGCGAGTGCGAGTGGACTCTGCCTTTGAGGCCCCACGCCGGGGACTTTGGCTACGCGGGGACTCTTTCCGGGGCTATGGCGTGGGCAA
MC55.32 BCY I  (661)  TGCATCGGCGAGTGCGAGTGGACTCTGCCTTTGAGGCCCCACGCCGGGGACTTTGGCTACGCGGGGACTCTTTCCGGGGCTATGGCGTGGGCAA
Consensus      (661)  TGCATCGGCGAGTGCGAGTGGACTCTGCCTTTGAGGCCCCACGCCGGGGACTTTGGCTACGCGGGGACTCTTTCCGGGGCTATGGCGTGGGCAA

                                                                                                              880
original BCY1  (768)  GCAGGATGTGTACTACGGCGTGGCCGAGACTAGCCCCGTGTGGGCGGCCAGGAGAACGCCACGCCCACCTTCCGTGCTCTTCTCCTGCTCCTCCTCT
MC50A19 BCY I  (771)  GCAGGATGTGTACTACGGCGTGGCCGAGACTAGCCCCGTGTGGGCGGCCAGGAGAACGCCACGCCCACCTTCCGTGCTCTTCTCCTGCTCCTCCTCTCCTCCTCCT
MC50A6 BCY I   (771)  GCAGGATGTGTACTACGGCGTGGCCGAGACTAGCCCCGTGTGGGCGGCCAGGAGAACGCCACGCCCACCTTCCGTGCTCTTCTCCTGCTCCTCCTCTCCTCCTCCT
MC50A8 BCY I   (771)  GCAGGATGTGTACTACGGCGTGGCCGAGACTAGCCCCGTGTGGGCGGCCAGGAGAACGCCACGCCCACCTTCCGTGCTCTTCTCCTGCTCCTCCTCTCCTCCTCCT
MC54.21 BCY I  (771)  GCAGGATGTGTACTACGGCGTGGCCGAGACTAGCCCCGTGTGGGCGGCCAGGAGAACGCCACGCCCACCTTCCGTGCTCTTCTCCTGCTCCTCYKCCTCCTCCTCCT
MC55.29 BCY I  (771)  GCAGGATGTGTACTACGGCGTGGCCGAGACTAGCCCCGTGTGGGCGGCCAGGAGAACGCCACGCCCACCTTCCGTGCTCTTCTCCTGCTCCTCCTCTCCTCCTCCT
MC55.32 BCY I  (771)  GCAGGATGTGTACTACGGCGTGGCCGAGACTAGCCCCGTGTGGGCGGCCAGGAGAACGCCACGCCCACCTTCCGTGCTCTTCTCCTGCTCCTCCTCTCCTCCTCCT
Consensus      (771)  GCAGGATGTGTACTACGGCGTGGCCGAGACTAGCCCCGTGTGGGCGGCCAGGAGAACGCCACGCCCACCTTCCGTGCTCTTCTCCTGCTCCTCCTCTCCTCCTCCT
```

FIGURE 3A

```
                        881                                                                                             990
original BCY1  ( 878)  CTTCCGCCAAGGCCCGCGCTGGGCGCCCCCGGGGCGCGCTGGGCGCCCCCGGGGCGCGCTGGGCGCCCCCGGGGCGCACACCGCTCCCCTGCCACTTCCGCGGGGACCCGAGCTGGCCGGACCCGAGCTGGCCGGACCCGAGCTGGCCGGAGAGCGCCCCCGGGGAGAGCCGCTCCCRG
MC50A19 BCY I  ( 881)  CTTCCGCCAAGGCCCGCGCTGGGCGCCCCCGGGGCGCGCTGGGCGCCCCCGGGGCGCACACCGCTCCCCTGCCACTTCCGCGGGGACCCGAGCTGGCCGGACCCGAGCTGGCCGGAGAGCGCCCCCGGGGAGAGCCGCTCCCAG
MC50A6 BCY I   ( 881)  CTTCCGCCAAGGCCCGCGCTGGGCGCCCCCGGGGCGCGCTGGGCGCCCCCGGGGCGCACACCGCTCCCCTGCCACTTCCGCGGGGACCCGAGCTGGCCGGACCCGAGCTGGCCGGAGAGCGCCCCCGGGGAGAGCCGCTCCCAG
MC50A8 BCY I   ( 881)  CTTCCGCCAAGGCCCGCGCTGGGCGCCCCCGGGGCGCGCTGGGCGCCCCCGGGGCGCACACCGCTCCCCTGCCACTTCCGCGGGGACCCGAGCTGGCCGGACCCGAGCTGGCCGGAGAGCGCCCCCGGGGAGAGCCGCTCCCAG
MC54.21 BCY I  ( 881)  CTTCCGCCAAGGCCCGCGCTGGGCGCCCCCGGGGCGCGCTGGGCGCCCCCGGGGCGCACACCGCTCCCCTGCCACTTCCGCGGGGACCCGAGCTGGCCGGACCCGAGCTGGCCGGAGAGCGCCCCCGGGGAGAGCCGCTCCCAG
MC55.29 BCY I  ( 881)  CTTCCGCCAAGGCCCGCGCTGGGCGCCCCCGGGGCGCGCTGGGCGCCCCCGGGGCGCACACCGCTCCCCTGCCACTTCCGCGGGGACCCGAGCTGGCCGGACCCGAGCTGGCCGGAGAGCGCCCCCGGGGAGAGCCGCTCCCAG
MC55.32 BCY I  ( 881)  CTTCCGCCAAGGCCCGCGCTGGGCGCCCCCGGGGCGCGCTGGGCGCCCCCGGGGCGCACACCGCTCCCCTGCCACTTCCGCGGGGACCCGAGCTGGCCGGACCCGAGCTGGCCGGAGAGCGCCCCCGGGGAGAGCCGCTCCCAG
Consensus      ( 881)  CTTCCGCCAAGGCCCGCGCTGGGCGCCCCCGGGGCGCACACCGCTCCCCTGCCACTTCCGCGGGGACCCGAGCTGGCCGGAGAGCGCCCCCGGGGAGAGCCGCTCCCAG

                        991                                                                                            1100
original BCY1  ( 988)  GGCTTCTCTAAACTTGGTGGGGGCGGCCTGCCGGAGCCCCGCCCCGG---CGGCGGCGGGATTGCATGGTCTGCTTTGAGAGCGAAGTGACTGCCGCCCTTGTGCCCTGCGGACA
MC50A19 BCY I  ( 991)  GGCTTCTCTAAACTTGGTGGGGGCGGCCTGCCGGAGCCCCGCCCCGG---CGGCGGCGGGATTGCATGGTCTGCTTTGAGAGCGAAGTGACTGCCGCCCTTGTGCCCTGCGGACA
MC50A6 BCY I   ( 991)  GGCTTCTCTAAACTTGGTGGGGGCGGCCTGCCGGAGCCCCGCCCCGG---CGGCGGCGGGATTGCATGGTCTGCTTTGAGAGCGAAGTGACTGCCGCCCTTGTGCCCTGCGGACA
MC50A8 BCY I   ( 991)  GGCTTCTCTAAACTTGGTGGGGGCGGCCTGCCGGAGCCCCGCCCCGG---CGGCGGCGGGATTGCATGGTCTGCTTTGAGAGCGAAGTGACTGCCGCCCTTGTGCCCTGCGGACA
MC54.21 BCY I  ( 991)  GGCTTCTCTAAACTTGGTGGGGGCGGCCTGCCGGAGCCCCGCCCCGG---CGGCGGCGGGATTGCATGGTCTGCTTTGAGAGCGAAGTGACTGCCGCCCTTGTGCCCTGCGGACA
MC55.29 BCY I  ( 991)  GGCTTCTCTAAACTTGGTGGGGGCGGCCTGCCGGAGCCCCGCCCCGG---CGGCGGCGGGATTGCATGGTCTGCTTTGAGAGCGAAGTGACTGCCGCCCTTGTGCCCTGCGGACA
MC55.32 BCY I  ( 991)  GGCTTCTCTAAACTTGGTGGGGGCGGCCTGCCGGAGCCCCGCCCCGG---CGGCGGCGGGATTGCATGGTCTGCTTTGAGAGCGAAGTGACTGCCGCCCTTGTGCCCTGCGGACA
Consensus      ( 991)  GGCTTCTCTAAACTTGGTGGGGGCGGCCTGCCGGAGCCCCGCCCCGG   CGGCGGCGGGATTGCATGGTCTGCTTTGAGAGCGAAGTGACTGCCGCCCTTGTGCCCTGCGGACA

                        1101                                                                                           1210
original BCY1  (1098)  CAACCTGTTCTGCATGGAGTGTGCAGTACGCATCTGCGAGAGGACGACCCCAGAGTGTCCCGTCTGCCACATCACAGCCAAGCCATCCGAATATTCTCCTAA---------------------
MC50A19 BCY I  (1098)  CAACCTGTTCTGCATGGAGTGTGCAGTACGCATCTGCGAGAGGACGACCCCAGAGTGTCCCGTCTGCCACATCACAGCCAAGCCATCCGAATATTCTCCTAAGGAT
MC50A6 BCY I   (1098)  CAACCTGTTCTGCATGGAGTGTGCAGTACGCATCTGCGAGAGGACGACCCCAGAGTGTCCCGTCTGCCACATCACAGCCAAGCCATCCGAATATTCTCCTAAGGAT
MC50A8 BCY I   (1098)  CAACCTGTTCTGCATGGAGTGTGCAGTACGCATCTGCGAGAGGACGACCCCAGAGTGTCCCGTCTGCCACATCACAGCCAAGCCATCCGAATATTCTCCTAAGGAT
MC54.21 BCY I  (1098)  CAACCTGTTCTGCATGGAGTGTGCAGTACGCATCTGCGAGAGGACGACCCCAGAGTGTCCCGTCTGCCACATCACAGCCAAGCCATCCGAATATTCTCCTAAGGAT
MC55.29 BCY I  (1098)  CAACCTGTTCTGCATGGAGTGTGCAGTACGCATCTGCGAGAGGACGACCCCAGAGTGTCCCGTCTGCCACATCACAGCCAAGCCATCCGAATATTCTCCTAA----
MC55.32 BCY I  (1098)  CAACCTGTTCTGCATGGAGTGTGCAGTACGCATCTGCGAGAGGACGACCCCAGAGTGTCCCGTCTGCCACATCACAGCCAAGCCATCCGAATATTCTCCTAA----
Consensus      (1101)  CAACCTGTTCTGCATGGAGTGTGCAGTACGCATCTGCGAGAGGACGACCCCAGAGTGTCCCGTCTGCCACATCACAGCCAAGCCATCCGAATATTCTCCTAA

                        1211                      1248
original BCY1  (1204)  -----------------------------------
MC50A19 BCY I  (1208)  CCACTAGTCCAGTGTGGTGGAATTCTGCAGATATCCA-
MC50A6 BCY I   (1208)  CCACTAGTCCAGTGTGGTGGAATTCTGCAGATATCCA-
MC50A8 BCY I   (1208)  CCACTAGTCCAGTGTGGTGGAATTCTGCAGATATCCA-
MC54.21 BCY I  (1204)  -----------------------------------
MC55.29 BCY I  (1204)  -----------------------------------
MC55.32 BCY I  (1204)  -----------------------------------
Consensus      (1211)  -----------------------------------
```

FIGURE 3B

```
MAELRLKGSS NTTECVPVPT SEHVAEIVGR QGCKIKALRA KTNTYIKTPV RGEEPVFMVT GRREDVATAR REIISAAEHF SMIRASRNKS
GAAFGVAPAL PGQVTIRVRV PYRVVGLVVG PKGATIKRIQ QQTNTYIITP SRDRDPVFEI TGAPGNVERA REEIETHIAV RTGKILEYNN
ENDFLAGSPD AAIDSRYSDA WRVHQPGCKP LSTFRQNSLG CIGECGVDSG FEAPRLGEQG GDFGYGGYLF PGYGVGKQDV YYGVAETSPP
LWAGQENATP TSVLFSSASS SSSSSAKARA GPPGAHRSPA TSAGPELAGL PRRPPGEPLQ GFSKLGGGGL RSPGGGRDCM VCFESEVTAA
LVPCGHNLFC MECAVRICER TDPECPVCHI TAAQAIRIFS
```